

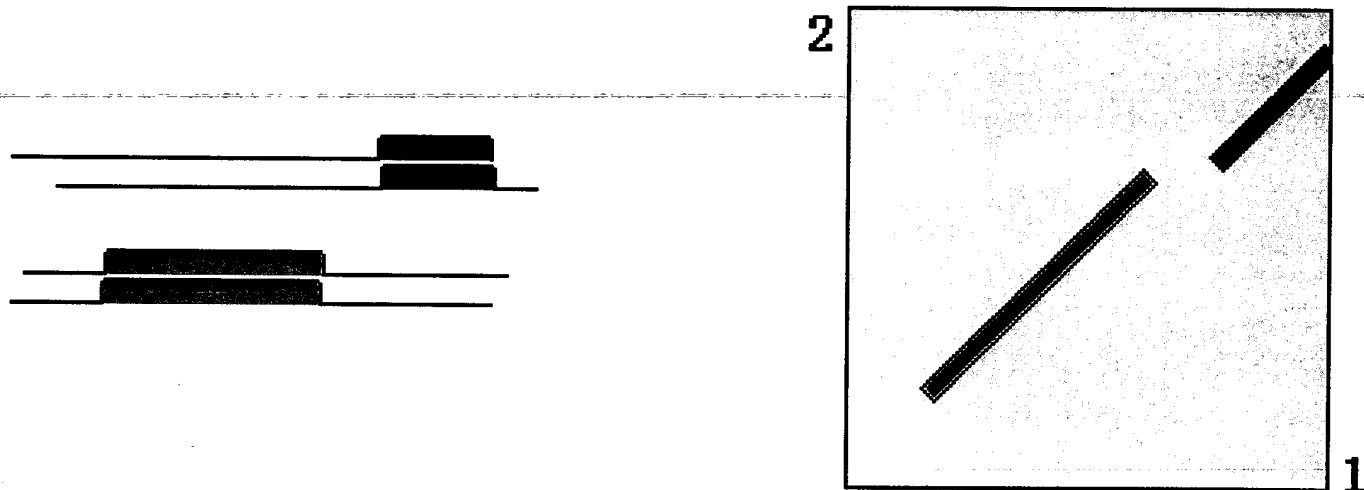


FORMAL DRAWING

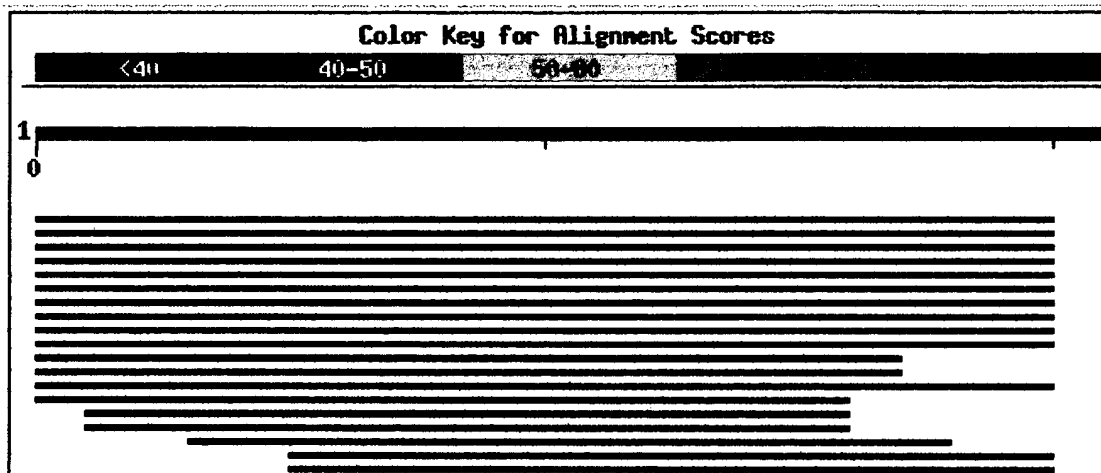
Fig. 5. BLAST search for two sequence alignment

Sequence 1 lcl|seq_1 Length 651 (1 .. 651)

Sequence 2 lcl|seq_2 Length 649 (1 .. 649)



940,610 sequences; 3,756,702,104 total letters



Sequences producing significant alignments:

Score E
(bits) Value

gi 13702791 gb AC006590.11 AC006590	Drosophila melanogaster...	42	0.003
gi 13702790 gb AC008184.4 AC008184	Drosophila melanogaster,...	42	0.003
gi 11094921 gb AC084471.1 AC084471	Caenorhabditis briggsae ...	42	0.003
gi 10799037 gb AF274345.1 AF274345	Caenorhabditis elegans l...	42	0.003
gi 7298444 gb AE003659.1 AE003659	Drosophila melanogaster g...	42	0.003
gi 15212042 emb AL158152.18 AL158152	Human DNA sequence fro...	42	0.003
gi 7211739 gb AF210771.1 AF210771	Caenorhabditis briggsae l...	42	0.003
gi 1229025 emb Z70203.1 CEC05G5	Caenorhabditis elegans cosm...	42	0.003
gi 4826511 emb AL049853.1 HS695020B	Human DNA sequence from...	42	0.003
gi 14189751 dbj AP001359.4 AP001359	Homo sapiens genomic DN...	42	0.003

Alignments

>gi|13702791|gb|AC006590.11|AC006590 Drosophila melanogaster, chromosome 2L, region 36E-, BAC clone
BACR13N02, complete sequence
Length = 172479

Score = 42.1 bits (21), Expect = 0.003

Identities = 21/21 (100%)

Strand = Plus / Plus

Query: 1 tgaggtagtaggttgatatagt 21

| | | | | | |

Sbjct: 37997 tgaggtagtaggttgatatagt 38017

Fig 7. The cleavage patterns are detected with MUSCA pattern discovery tool. From this gene, most derivative sequences of the cleavage center could be found and used for predicting specific and efficacious sequences. The corresponding results were listed in table 4.

NM_032387.1 GI:15277311, Homo sapiens protein kinase, lysine deficient 4 (PRKWINK4), mRNA

```

1  gccctgctct ttcctcatgt tggcaatccc cggccaacga gaccacgctc ctcattgtcc
61 agactgaggc cgacctggcc ctgcggcccc cgcctcctct tggcaccgag ggcagcccc
121 gccctgctct cctcctctgc cgagcgcgcc gcttctctgc caaggetgag ccccgccgc
181 gctcttctcg tctcagccgc cgtagctcag tgcacttggg gctgctgagc tcttggtccc
241 tgcagcctc acccgctcgc gacccccccg atcctcgcga ctccgctggt cctggccccg
301 cgaggagccc accgcctagc tccaaagaac ccccgaggag caagtggacc gaggagcccc
361 ctgtgaagcg tgcgaagac tccgcgcgtc ccgagctccc ggaactctga gtgggccccg
421 cgtccaggga gccgctaagg gtccctgaag ctgtggccct agagcggcgg cgggagcagg
481 aagaaaagga ggacatggag acccaggctg tggcaacgct ccccgatggc cgatacctca
541 agtttgacat cgagattgga cgtggctcct tcaagacggt gtatcgaggg ctgacacccg
601 acaccacagt ggaggtggcc tgggtgtgag tgcagactcc gaaactgtct agagctgagc
661 ggcagcgctt ctcagaggag gtggagatgc tcaaggggct gcagcaccac aacatcgctc
721 gcttctatga ttcggtgaag tccgtgctga ggggcccagg ttgcatcggt ctggtcacccg
781 aactcatgac ctccggcacc ctcaagacgt acctgaggcg gttccgggag atgaagccgc
841 cgtctcttca gcgctggagc cgcctaatcc tggggcgact tcatttctca cactcccgcc
901 ttctctccat cctgcacccg catctcaagt ggcacaatgt ctttatcagc gacactactg
961 gctctgtcaa aatcggggac ctgggcctgg ccacgctcaa gcgcgcctcc tttgccaaag
1021 gtgtcatccg gaccccgcaa ttcattggcc ccgagatgta cgaggaaaag tacgatgagg
1081 ccgtggacgt gtacgcgttc ggcatgtgca tgcctggagat ggccacctct gactacctgt
1141 actccgagtg ccagaatgcc gcgcaaatct accgcaaggt cacttcggcc agaaagccga
1201 acagcttcca caaggtgaag atacccgagg tgaaggagat cattgaaggc tgcacccgca
1261 cggataagaa cgagaggttc accatccagg acctcctggc ccacgccttc ttcgcgagg
1321 agcgcggtgt gacgtggaa ctagcggagg aggacgacgg cgagaagccg gctctcaagc
1381 tctggtctcg catggaggac gcgcggcgcg gggggcgccc accgcacaac caggccatcg
1441 agttcctgtt ccagctgggc cgcgacggcg ccgaggaggt ggcacaggag atggtggctc
1501 tgggcttggg ctgtgaagcc gattaccagc cagtggcccc tgcagtacgt gaacgggttg
1561 ctgccatcca gcgaaagcg gagaagctgc gtaaagcaag ggaattggag gcactccac
1621 cagagccagg acctccacca gcaactgtgc ccatggcccc cgttccccc agtgtcttcc
1681 cccctgagcc tgaggagcca gaggcagacc agcaccagcc ctctcttttc cggcacgcca
1741 gctactcacc taccatttcg gattgcgaga ctgatggcta cctcagctcc tccggttcc

```

Fig 8. Evaluation of an amyloid SDSO designed with the specific cleavage pattern method.

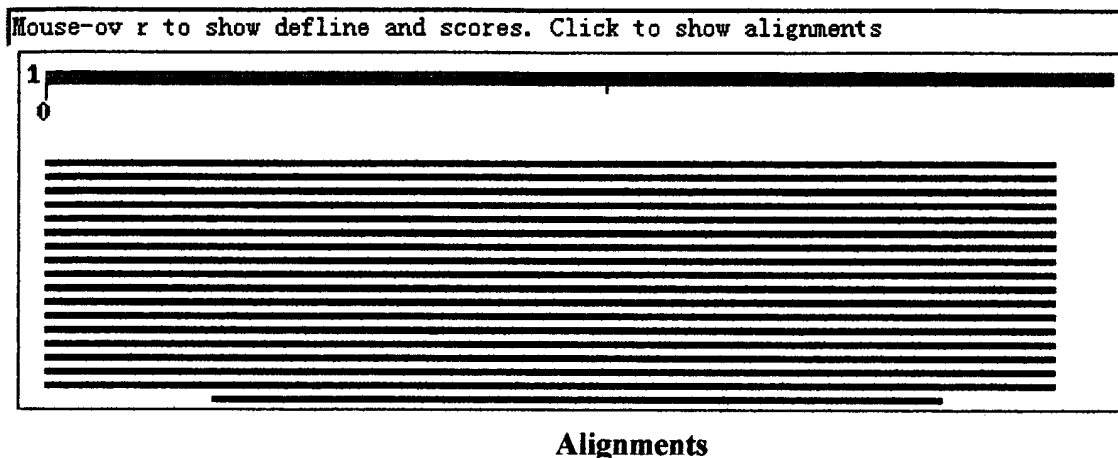
RID: 1000513225-8517-5028

Query= (19 letters)

Database: nt 951,499 sequences; 3,985,165,516 total letters

>gi14780094|ref|XM_009710.2| Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA Length = 1708

Distribution of 18 Blast Hits on the Query Sequence



Score = 38.2 bits (19), Expect = 0.007

Identities = 19/19 (100%)

Strand = Plus / Plus

Query: 1 tcagttacggaaacgatgc 19

||||| ||| ||| ||| |||

Sbjct: 669 tcagttacggaaacgatgc 687

Fig. 9 Diagram of gene drugs

Fig. 9A illustrated a large unilamellar vesicles (LUVs), in which there are many different SDSO molecules (red) and branched 25 kDa polyethylenimine (PEI) or spermidine (gray) and on which there is a targeting molecule (purple). Fig. 9B depicted many small unilamellar vesicles (SUVs) in blue color, outside of which there are many SDSO molecules (red). Fig. 9C showed the relations of SDSO molecules (red) and branched 25 kDa polyethylenimine (PEI) or spermidine (gray).

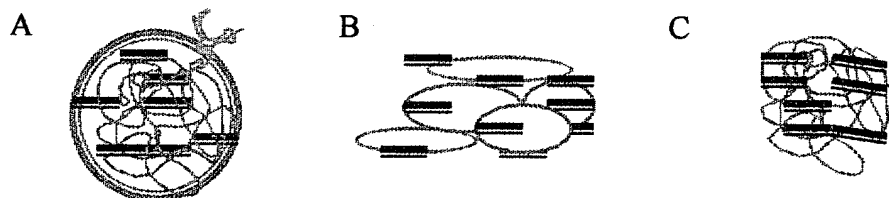
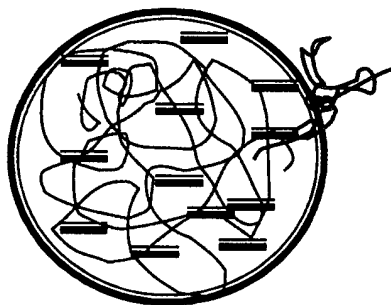


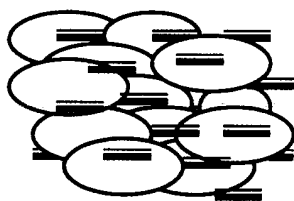
Fig 10. The inhibitory effects of Dermogene on the survival and proliferation of human melanoma cells.

Fig. 9 Diagram of gene drugs

A



B



C

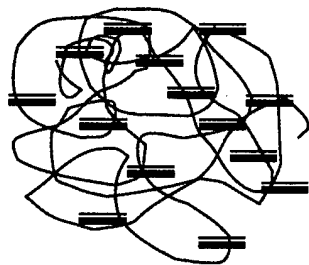




Fig 10. The inhibitory effects of Dermogene on the survival and proliferation of human melanoma cells.

Effects of Dermogene on Melanoma Cells

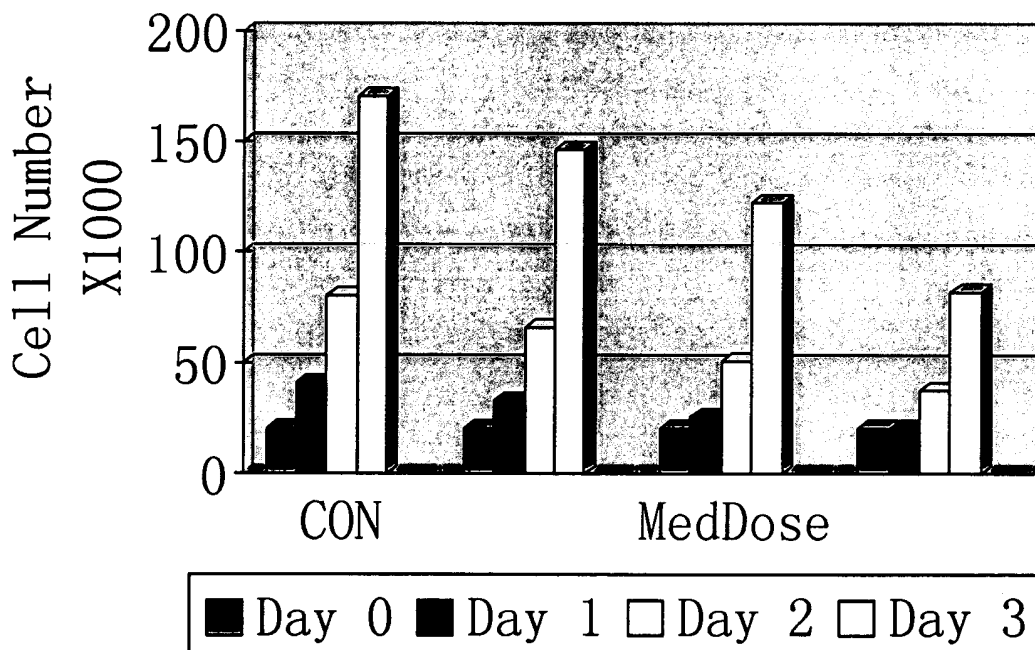




Fig 11. The in vitro effects of Dermogene on the survival and proliferation of human melanoma cells.

Effects of Dermogene on the proliferation
of melanoma cells

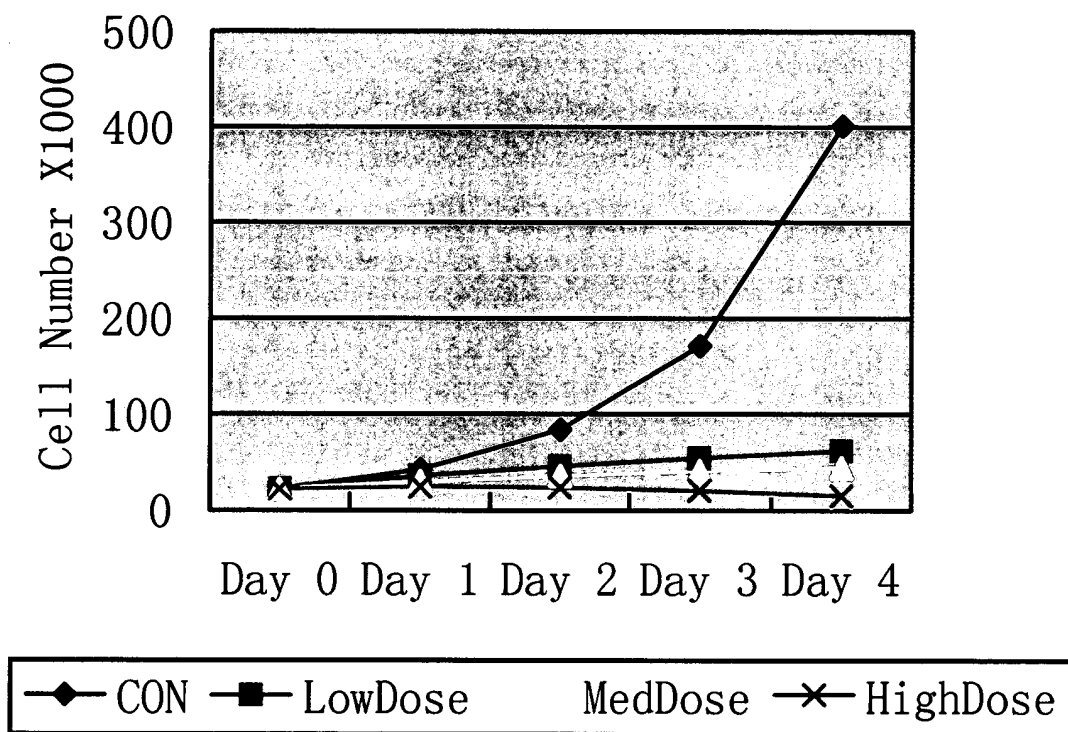


Fig 12. In vivo pharmaceutical effects of Dermogene on melanoma cells.

In Vivo Effects of siRNAs on Melanoma Cells

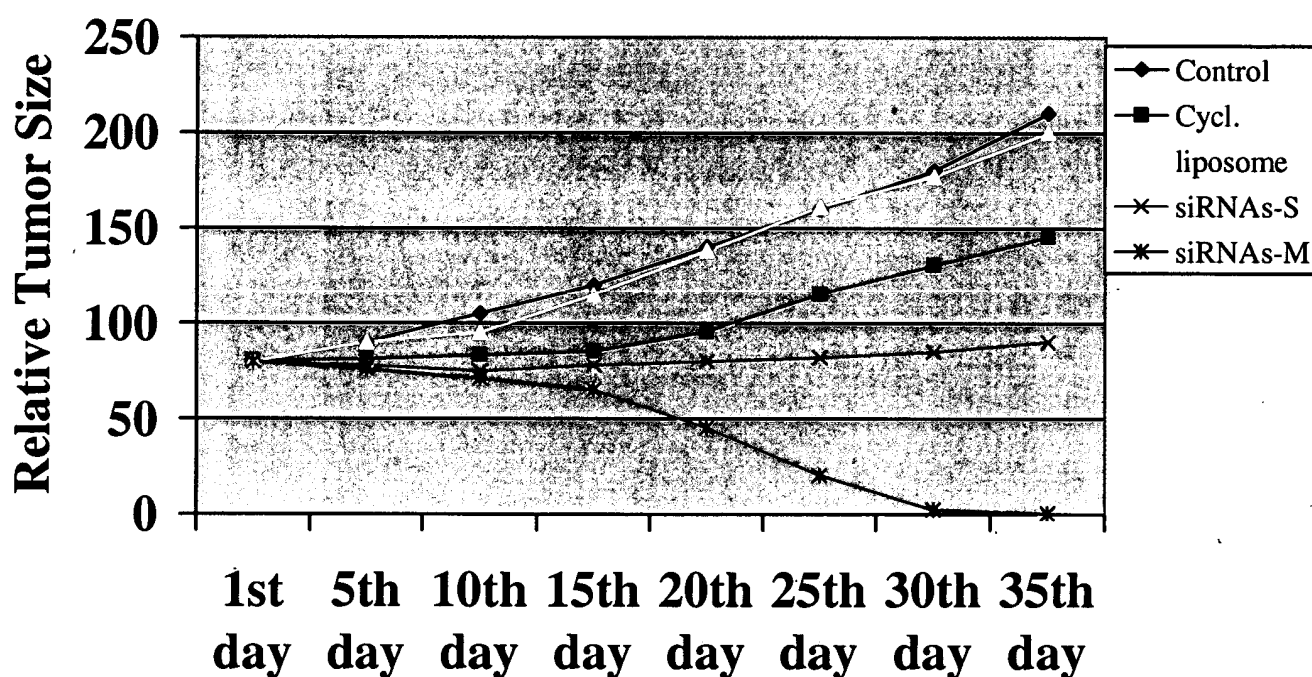




Fig.13. The biological roles of Leukogene on CML cells.

